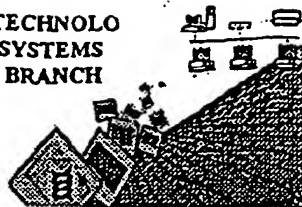# RAW SEQUENCE LISTING
ERROR REPORT

**BIOTECHNOLO
SYSTEMS
BRANCH**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: US 10 799,320
Source: TWO
Date Processed by STIC: 7/7/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 4.2 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):
   U.S. Patent and Trademark Office, 220 20th Street S.; Customer Window; Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Revised 05/17/04

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 10/799,320

1 _____ Wrapped Nucleics
Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 _____ Invalid Line Length
The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 _____ Misaligned Amino
Numbering
The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 _____ Non-ASCII
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 _____ Variable Length
Sequence(s)_____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 _____ PatentIn 2.0
"bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 _____ Skipped Sequences
(OLD RULES)
Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 _____ Skipped Sequences
(NEW RULES)
Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
<210> sequence id number
<400> sequence id number
000

9 _____ Use of n's or Xaa's
(NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 _____ Invalid <213>
Response
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 _____ Use of <220>
Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 _____ PatentIn 2.0
"bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 _____ Misuse of n/Xaa
"n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid

IFWO

RAW SEQUENCE LISTING   DATE: 07/07/2004
PATENT APPLICATION: US/10/799,320   TIME: 15:38:12

Input Set : A:\2500us1p.ST25.txt
Output Set: N:\CRF4\07072004\J799320.raw

```
  3 <110> APPLICANT: SAIKAWA, Akira
  4        IGARI, Yasutaka
  5        HATA, Yoshio
  6        YAMAMOTO, Kazumichi
  8 <120> TITLE OF INVENTION: Sustained-Release Composition, Method of its Preparation and
Use Thereof
 10 <130> FILE REFERENCE: 2500US1P
W--> 11 <140> CURRENT APPLICATION NUMBER: 10/799,320
 12 <141> CURRENT FILING DATE: 2004-03-12
 15 <150> PRIOR APPLICATION NUMBER: 09/582,926
 16 <151> PRIOR FILING DATE: 2000-07-05
 18 <150> PRIOR APPLICATION NUMBER: PCT/JP99/00086
 19 <151> PRIOR FILING DATE: 1999-01-13
 21 <150> PRIOR APPLICATION NUMBER: JP 10-6412
 22 <151> PRIOR FILING DATE: 1998-01-16
 24 <160> NUMBER OF SEQ ID NOS: 5
 26 <170> SOFTWARE: PatentIn version 3.0
```

Does Not Comply
Corrected Diskette Needed
(pg. 1)

ERRORED SEQUENCES

```
214 <210> SEQ ID NO: 5
215 <211> LENGTH: 11
216 <212> TYPE: PRT
217 <213> ORGANISM: artificial
219 <220> FEATURE:
220 <223> OTHER INFORMATION: LH-RH derived peptides
222 <220> FEATURE:
223 <221> NAME/KEY: MOD_RES
224 <222> LOCATION: (1)..(1)
225 <223> OTHER INFORMATION: X is 5-oxo carboxy terminal
228 <220> FEATURE:
229 <221> NAME/KEY: MOD_RES
230 <222> LOCATION: (7)..(7)
231 <223> OTHER INFORMATION: X is DLeu
234 <220> FEATURE:
235 <221> NAME/KEY: MOD_RES
236 <222> LOCATION: (11)..(11)
237 <223> OTHER INFORMATION: X is NH-C2H5 amino terminal
240 <400> SEQUENCE: 5
W--> 242 Xaa Pro His Trp Ser Tyr Xaa Leu Arg Pro Xaa
243 1               5                    10
E--> 248 (5)  delete
```

Pls see item
 # 13 on error
= summary sheet

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 07/07/2004
PATENT APPLICATION: US/10/799,320   TIME: 15:38:13

Input Set : A:\2500us1p.ST25.txt
Output Set: N:\CRF4\07072004\J799320.raw

Invalid Line Length:
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 8

Invalid <213> Response:
Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,2,3,4,5

VERIFICATION SUMMARY
PATENT APPLICATION: US/10/799,320

DATE: 07/07/2004
TIME: 15:38:13

Input Set : **A:\2500us1p.ST25.txt**
Output Set: **N:\CRF4\07072004\J799320.raw**

```
L:11 M:283 W: Missing Blank Line separator, <140> field identifier
L:57 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0
L:119 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0
L:150 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
L:211 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0
L:242 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0
L:248 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:5
```